

SEQUENCE LISTING

SEQ. ID No. 1

LENGTH: 271

TYPE: amino acid

5

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro
1 5 10 15
Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr
20 25 30
Gly Tyr Arg Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met
35 40 45
15 Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser
50 55 60
Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu
65 70 75
Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val Val Thr Thr
20 80 85 90
Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val Thr Asp Ala
95 100 105
Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr
110 115 120

Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr
125 130 135
Pro Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile
140 145 150
5 Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr
155 160 165
Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser
170 175 180
Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr
10 185 190 195
Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile
200 205 210
Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg
215 220 225
15 Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile
230 235 240
Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala
245 250 255
Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys
20 260 265 270
Thr

SEQ. ID No. 2

LENGTH: 25

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

5 Asp Glu Leu Pro Gln Leu Val Thr Leu Pro His Pro Asn Leu His
1 5 10 15
Gly Pro Glu Ile Leu Asp Val Pro Ser Thr
20 25

SEQ. ID No. 3

10 LENGTH: 155

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

15 SEQUENCE:

Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp
1 5 10 15
Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys
20 25 30
20 Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro
35 40 45
Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile
50 55 60
Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys

65 70 75

Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg

80 85 90

Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu

5 95 100 105

Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr

110 115 120

Thr Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu

125 130 135

10 Gly Ser Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro

140 145 150

Met Ser Ala Lys Ser

155

15 SEQ. ID No. 4

LENGTH: 432

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

20 SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
35 40 45
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu
50 55 60
5 Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln
65 70 75
His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp
80 85 90
Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe
10 95 100 105
Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg
110 115 120
Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp
125 130 135
15 Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr
140 145 150
Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg
155 160 165
Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp
20 170 175 180
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu
185 190 195
Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg
200 205 210
25 Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe

| | | | |
|----|---|-----|-----|
| | 215 | 220 | 225 |
| | Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys | | |
| | 230 | 235 | 240 |
| | Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg | | |
| 5 | 245 | 250 | 255 |
| | Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg | | |
| | 260 | 265 | 270 |
| | Thr Glu Ile Asp Lys Pro Ser Met Ala Ala Gly Ser Ile Thr Thr | | |
| | 275 | 280 | 285 |
| 10 | Leu Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro | | |
| | 290 | 295 | 300 |
| | Gly His Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly | | |
| | 305 | 310 | 315 |
| | Phe Phe Leu Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg | | |
| 15 | 320 | 325 | 330 |
| | Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu | | |
| | 335 | 340 | 345 |
| | Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu | | |
| | 350 | 355 | 360 |
| 20 | Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys Val Thr | | |
| | 365 | 370 | 375 |
| | Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr Asn | | |
| | 380 | 385 | 390 |
| | Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys | | |
| 25 | 395 | 400 | 405 |

Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln
410 415 420
Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
425 430

5 SEQ. ID NO. 5

LENGTH: 457

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

10 MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg
1 5 10 15
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
20 25 30
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
35 40 45
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu
50 55 60
20 Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln
65 70 75
His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp
80 85 90
Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

| | | | |
|----|---|-----|-----|
| | 95 | 100 | 105 |
| | Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg | | |
| | 110 | 115 | 120 |
| | Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp | | |
| 5 | 125 | 130 | 135 |
| | Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr | | |
| | 140 | 145 | 150 |
| | Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg | | |
| | 155 | 160 | 165 |
| 10 | Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp | | |
| | 170 | 175 | 180 |
| | Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu | | |
| | 185 | 190 | 195 |
| | Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg | | |
| 15 | 200 | 205 | 210 |
| | Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe | | |
| | 215 | 220 | 225 |
| | Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys | | |
| | 230 | 235 | 240 |
| 20 | Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg | | |
| | 245 | 250 | 255 |
| | Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg | | |
| | 260 | 265 | 270 |
| | Thr Glu Ile Asp Lys Pro Ser Met Ala Ala Gly Ser Ile Thr Thr | | |
| 25 | 275 | 280 | 285 |

Leu Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro
290 295 300
Gly His Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly
305 310 315
5 Phe Phe Leu Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg
320 325 330
Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu
335 340 345
Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu
10 350 355 360
Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys Val Thr
365 370 375
Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr Asn
380 385 390
15 Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
395 400 405
Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln
410 415 420
Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Ala Ser Asp Glu Leu
20 425 430 435
Pro Gln Leu Val Thr Leu Pro His Pro Asn Leu His Gly Pro Glu
440 445 450
Ile Leu Asp Val Pro Ser Thr
455

SEQ. ID No. 6

LENGTH: 186

TYPE: amino acid

STRANDEDNESS: single

5

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Gly Ile Arg Gly Leu Lys Gly Thr Lys Gly Glu Lys Gly Glu Asp
1 5 10 15
Gly Phe Pro Gly Phe Lys Gly Asp Met Gly Ile Lys Gly Asp Arg
10 20 25 30
Gly Glu Ile Gly Pro Pro Gly Pro Arg Gly Glu Asp Gly Pro Glu
35 40 45
Gly Pro Lys Gly Arg Gly Pro Asn Gly Asp Pro Gly Pro Leu
50 55 60
Gly Pro Pro Gly Glu Lys Gly Lys Leu Gly Val Pro Gly Leu Pro
65 70 75
Gly Tyr Pro Gly Arg Gln Gly Pro Lys Gly Ser Ile Gly Phe Pro
80 85 90
20 Gly Phe Pro Gly Ala Asn Gly Glu Lys Gly Gly Arg Gly Thr Pro
95 100 105
Gly Lys Pro Gly Pro Arg Gly Gln Arg Gly Pro Thr Gly Pro Arg
110 115 120
Gly Glu Arg Gly Pro Arg Gly Ile Thr Gly Lys Pro Gly Pro Lys
25 125 130 135

Gly Asn Ser Gly Gly Asp Gly Pro Ala Gly Pro Pro Gly Glu Arg
140 145 150
Gly Pro Asn Gly Pro Gln Gly Pro Thr Gly Phe Pro Gly Pro Lys
155 160 165
5 Gly Pro Pro Gly Pro Pro Gly Lys Asp Gly Leu Pro Gly His Pro
170 175 180
Gly Gln Arg Gly Glu Thr
185

SEQ. ID No. 7

10 LENGTH: 464

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

15 SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg
1 5 10 15
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
20 25 30
20 Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
35 40 45
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu
50 55 60
Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

| | | | |
|----|---|-----|-----|
| | 65 | 70 | 75 |
| | His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp | | |
| | 80 | 85 | 90 |
| 5 | Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe | | |
| | 95 | 100 | 105 |
| | Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg | | |
| | 110 | 115 | 120 |
| 10 | Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp | | |
| | 125 | 130 | 135 |
| | Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr | | |
| | 140 | 145 | 150 |
| | Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg | | |
| | 155 | 160 | 165 |
| 15 | Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp | | |
| | 170 | 175 | 180 |
| | Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu | | |
| | 185 | 190 | 195 |
| | Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg | | |
| | 200 | 205 | 210 |
| 20 | Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe | | |
| | 215 | 220 | 225 |
| | Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys | | |
| | 230 | 235 | 240 |
| 25 | Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg | | |
| | 245 | 250 | 255 |

Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg
260 265 270
Thr Glu Ile Asp Lys Pro Ser Met Gly Ile Arg Gly Leu Lys Gly
275 280 285
5 Thr Lys Gly Glu Lys Gly Glu Asp Gly Phe Pro Gly Phe Lys Gly
290 295 300
Asp Met Gly Ile Lys Gly Asp Arg Gly Glu Ile Gly Pro Pro Gly
305 310 315
Pro Arg Gly Glu Asp Gly Pro Glu Gly Pro Lys Gly Arg Gly Gly
10 320 325 330
Pro Asn Gly Asp Pro Gly Pro Leu Gly Pro Pro Gly Glu Lys Gly
335 340 345
Lys Leu Gly Val Pro Gly Leu Pro Gly Tyr Pro Gly Arg Gln Gly
350 355 360
15 Pro Lys Gly Ser Ile Gly Phe Pro Gly Phe Pro Gly Ala Asn Gly
365 370 375
Glu Lys Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly
380 385 390
Gln Arg Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly
20 395 400 405
Ile Thr Gly Lys Pro Gly Pro Lys Gly Asn Ser Gly Gly Asp Gly
410 415 420
Pro Ala Gly Pro Pro Gly Glu Arg Gly Pro Asn Gly Pro Gln Gly
425 430 435
25 Pro Thr Gly Phe Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly

440

445

450

Lys Asp Gly Leu Pro Gly His Pro Gly Gln Arg Gly Glu Thr

455

460

SEQ. ID No. 8

5

LENGTH: 489

10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

35 40 45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu

50 55 60

Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

65 70 75

His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp

80 85 90

Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

95 100 105

Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg
110 115 120

Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp
125 130 135

5 Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr
140 145 150

Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg
155 160 165

10 Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp
170 175 180

Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu
185 190 195

Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg
200 205 210

15 Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
215 220 225

Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys
230 235 240

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg
245 250 255

20 Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg
260 265 270

Thr Glu Ile Asp Lys Pro Ser Met Gly Ile Arg Gly Leu Lys Gly
275 280 285

25 Thr Lys Gly Glu Lys Gly Glu Asp Gly Phe Pro Gly Phe Lys Gly

| | | | |
|----|---|-----|-----|
| | 290 | 295 | 300 |
| | Asp Met Gly Ile Lys Gly Asp Arg Gly Glu Ile Gly Pro Pro Gly | | |
| | 305 | 310 | 315 |
| | Pro Arg Gly Glu Asp Gly Pro Glu Gly Pro Lys Gly Arg Gly Gly | | |
| 5 | 320 | 325 | 330 |
| | Pro Asn Gly Asp Pro Gly Pro Leu Gly Pro Pro Gly Glu Lys Gly | | |
| | 335 | 340 | 345 |
| | Lys Leu Gly Val Pro Gly Leu Pro Gly Tyr Pro Gly Arg Gln Gly | | |
| | 350 | 355 | 360 |
| 10 | Pro Lys Gly Ser Ile Gly Phe Pro Gly Phe Pro Gly Ala Asn Gly | | |
| | 365 | 370 | 375 |
| | Glu Lys Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly | | |
| | 380 | 385 | 390 |
| | Gln Arg Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly | | |
| 15 | 395 | 400 | 405 |
| | Ile Thr Gly Lys Pro Gly Pro Lys Gly Asn Ser Gly Gly Asp Gly | | |
| | 410 | 415 | 420 |
| | Pro Ala Gly Pro Pro Gly Glu Arg Gly Pro Asn Gly Pro Gln Gly | | |
| | 425 | 430 | 435 |
| 20 | Pro Thr Gly Phe Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly | | |
| | 440 | 445 | 450 |
| | Lys Asp Gly Leu Pro Gly His Pro Gly Gln Arg Gly Ala Ser Asp | | |
| | 455 | 460 | 465 |
| | Glu Leu Pro Gln Leu Val Thr Leu Pro His Pro Asn Leu His Gly | | |
| 25 | 470 | 475 | 480 |

Pro Glu Ile Leu Asp Val Pro Ser Thr

485

SEQ. ID No. 9

LENGTH: 36

5

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

10

AAACCATGGC AGTCAGCGAC GAGCTTCCCC AACTGG

36

SEQ. ID No. 10

LENGTH: 20

15

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AATTGACAAA CCATCCATGG

20

20

SEQ. ID No. 11

LENGTH: 33

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

CCATTA~~AA~~AT CAGCTAGCAG CAGACATTGG AAG

33

5

SEQ. ID No. 12

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

TCTAGAGGAT CCTTAGCTAG CGCCTCTCTG TCCAGG

36

10
9
8
7
6
5
4
3
2
1

SEQ. ID No. 13

LENGTH: 547

15

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

20

Ala Ala Ser Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln

5

10

15

Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn Val

20

25

30

5 Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu Lys Thr
35 40 45
Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser Val
50 55 60
Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser Val
65 70 75
Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val
80 85 90
Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val
95 100 105
Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys
110 115 120
Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn
125 130 135
15 Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser
140 145 150
Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr
155 160 165
Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val Ile
20 170 175 180
Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu
185 190 195
Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg
200 205 210
25 Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser

215 220 225
Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu
230 235 240
Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr
5 245 250 255
Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly
260 265 270
Arg Lys Lys Thr Ser Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe
275 280 285
Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro
290 295 300
Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu
305 310 315
Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser
320 325 330
Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val
335 340 345
Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln
350 355 360
20 Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala
365 370 375
Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg
380 385 390
Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro
25 395 400 405

5

Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val
410 415 420
Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys
425 430 435
Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val
440 445 450
Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg
455 460 465
Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro
470 475 480
Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro
485 490 495
Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val
500 505 510
Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr
515 520 525
Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu
530 535 540
Ile Gly Arg Lys Lys Thr Ser
20 545

SEQ. ID No. 14

LENGTH: 826

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Ala Ala Ser Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp

5 5 10 15

Thr Met Arg Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr

20 25 30

Asn Phe Leu Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val

35 40 45

Ala Glu Leu Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr

50 55 60

Asn Leu Leu Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val

65 70 75

Tyr Glu Gln His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr

80 85 90

Gly Leu Asp Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala

95 100 105

Asn Ser Phe Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr

110 115 120

20 Gly Tyr Arg Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro

125 130 135

Arg Glu Asp Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr

140 145 150

Asn Leu Thr Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu

25 155 160 165

Asn Gly Arg Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr
170 175 180
Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
185 190 195
5 Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg
200 205 210
Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
215 220 225
Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser
10 230 235 240
Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
245 250 255
Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile
260 265 270
15 Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Thr Ser Ala Ile Pro
275 280 285
Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu
290 295 300
Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg
20 305 310 315
Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile
320 325 330
Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser Gly Leu Met
335 340 345
25 Val Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr

5

10

15

20

25

| | | | |
|----|---|-----|-----|
| | 350 | 355 | 360 |
| | Leu Thr Ser Arg Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn | | |
| | 365 | 370 | 375 |
| | Val Ser Pro Pro Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr | | |
| 5 | 380 | 385 | 390 |
| | Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly | | |
| | 395 | 400 | 405 |
| | Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln | | |
| | 410 | 415 | 420 |
| 10 | Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu | | |
| | 425 | 430 | 435 |
| | Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp | | |
| | 440 | 445 | 450 |
| 15 | Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile | | |
| | 455 | 460 | 465 |
| | Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser | | |
| | 470 | 475 | 480 |
| | Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr | | |
| | 485 | 490 | 495 |
| 20 | Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val | | |
| | 500 | 505 | 510 |
| | Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu | | |
| | 515 | 520 | 525 |
| | Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn | | |
| 25 | 530 | 535 | 540 |

Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr Ser Ala
545 550 555
Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr
560 565 570
5 Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly
575 580 585
Tyr Arg Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys
590 595 600
Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser Gly
605 610 615
Leu Met Val Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu Lys
620 625 630
Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val Val Thr Thr Leu
635 640 645
Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val Thr Asp Ala Thr
650 655 660
Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr Ile
665 670 675
Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr Pro
20 680 685 690
Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr
695 700 705
Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu
710 715 720
25 Asn Asp Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr

725 730 735
Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro
740 745 750
Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr
5 755 760 765
Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu
770 775 780
Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr
785 790 795
Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu
800 805 810
Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr
815 820 825
Ser

15 SEQ. ID No. 15

LENGTH: 38

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

20 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCGCT ATTCCTGCAC CAACTGAC

38

SEQ. ID No. 16

5 LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAAGGATCCC TAACTAGTCT TTTTCCTTCC AATCAG

36

10 SEQ. ID No. 17

LENGTH: 1644

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an
artificial polypeptide)

15 SEQUENCE:

ATGGCAGCTA GCGCTATTCC TGCACCAACT GACCTGAAGT TCACTCAGGT CACACCCACA 60
AGCCTGAGCG CCCAGTGGAC ACCACCCAAT GTTCAGCTCA CTGGATATCG AGTGCGGGTG 120
ACCCCCAAGG AGAAGACCGG ACCAATGAAA GAAATCAACC TTGCTCCTGA CAGCTCATCC 180
GTGGTTGTAT CAGGACTTAT GGTGGCCACC AAATATGAAG TGAGTGTCTA TGCTCTTAAG 240
20 GACACTTTGA CAAGCAGACC AGCTCAGGGT GTTGTACCA CTCTGGAGAA TGTCAGCCCA 300
CCAAGAAGGG CTCGTGTGAC AGATGCTACT GAGACCACCA TCACCATTAG CTGGAGAAC 360
AAGACTGAGA CGATCACTGG CTTCCAAGTT GATGCCGTT CAGCCAATGG CCAGACTCCA 420
ATCCAGAGAA CCATCAAGCC AGATGTCAGA AGCTACACCA TCACAGGTTT ACAACCAGGC 480
ACTGACTACA AGATCTACCT GTACACCTTG AATGACAATG CTCGGAGCTC CCCTGTGGTC 540

ATCGACGCCCT CCACTGCCAT TGATGCACCA TCCAACCTGC GTTCCTGGC CACCACACCC 600
AATTCCCTTGC TGGTATCATG GCAGCCGCCA CGTGCCAGGA TTACCGGCTA CATCATCAAG 660
TATGAGAAGC CTGGGTCTCC TCCCAGAGAA GTGGTCCCTC GGCCCCGCCA TGGTGTACCA 720
GAGGCTACTA TTACTGGCCT GGAACCGGGA ACCGAATATA CAATTTATGT CATTGCCCTG 780
5 AAGAATAATC AGAAGAGCGA GCCCCTGATT GGAAGGAAAA AGACTAGCGC TATTCCCTGCA 840
CCAACTGACC TGAAGTTCAC TCAGGTACCA CCCACAAGCC TGAGCGCCCA GTGGACACCA 900
CCCAATGTTG AGCTCACTGG ATATCGAGTG CGGGTGACCC CCAAGGAGAA GACCGGACCA 960
ATGAAAGAAA TCAACCTTGC TCCTGACAGC TCATCCGTGG TTGTATCAGG ACTTATGGTG 1020
GCCACCAAAT ATGAAGTGAG TGTCTATGCT CTTAAGGACA CTTTGACAAG CAGACCAGCT 1080
CAGGGTGTG TCACCACTCT GGAGAATGTC AGCCCACCAA GAAGGGCTCG TGTGACAGAT 1140
GCTACTGAGA CCACCATCAC CATTAGCTGG AGAACCAAGA CTGAGACGAT CACTGGCTTC 1200
CAAGTTGATG CCGTTCCAGC CAATGGCCAG ACTCCAATCC AGAGAACCAT CAAGCCAGAT 1260
GTCAGAAGCT ACACCATCAC AGGTTACAA CCAGGCCTG ACTACAAGAT CTACCTGTAC 1320
ACCTTGAATG ACAATGCTCG GAGCTCCCT GTGGTCATCG ACGCCTCCAC TGCCATTGAT 1380
15 GCACCATCCA ACCTGCGTTT CCTGGCCACC ACACCCAATT CCTTGCTGGT ATCATGGCAG 1440
CCGCCACGTG CCAGGATTAC CGGCTACATC ATCAAGTATG AGAACCTGG GTCTCCCTCCC 1500
AGAGAAAGTGG TCCCTCGGCC CCGCCCTGGT GTCACAGAGG CTACTATTAC TGGCCTGGAA 1560
CCGGGAACCG AATATACAAT TTATGTCATT GCCCTGAAGA ATAATCAGAA GAGCGAGCCC 1620
CTGATTGGAA GGAAAAAGAC TAGT 1644
20 SEQ. ID No. 18
LENGTH: 37
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
25 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCCCC ACTGACCTGC GATTCAC

37

SEQ. ID No. 19

LENGTH: 38

5 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAAAGATCTC TAACTAGTGG ATGGTTTGTC AATTCTG

38

SEQ. ID No. 20

LENGTH: 2481

TYPE: nucleic acid

STRANDEDNESS: double

15 TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptyide)

SEQUENCE:

ATGGCAGCTA GCCCCACTGA CCTGCGATTC ACCAACATTG GTCCAGACAC CATGCGTGT 60

20 ACCTGGGCTC CACCCCCATC CATTGATTAA ACCAACTTCC TGGTGCCTTA CTCACCTGTG 120

AAAAATGAGG AAGATGTTGC AGAGTTGTCA ATTTCTCCTT CAGACAATGC AGTGGTCTTA 180

ACAAATCTCC TGCCTGGTAC AGAATATGTA GTGAGTGTCT CCAGTGTCTA CGAACACAT 240

GAGAGCACAC CTCTTAGAGG AAGACAGAAA ACAGGTCTTG ATTCCCCAAC TGGCATTGAC 300

TTTTCTGATA TTACTGCCAA CTCTTTACT GTGCACTGGA TTGCTCCTCG AGCCACCATC 360
ACTGGCTACA GGATCCGCCA TCATCCCGAG CACTTCAGTG GGAGACCTCG AGAAGATCGG 420
GTGCCCCACT CTCGGAATTC CATCACCCCTC ACCAACCTCA CTCCAGGCAC AGAGTATGTG 480
GTCAGCATCG TTGCTCTTAA TGGCAGAGAG GAAAGTCCCT TATTGATTGG CCAACAATCA 540
5 ACAGTTCTG ATGTTCCGAG GGACCTGGAA GTTGTGCTG CGACCCCCAC CAGCCTACTG 600
ATCAGCTGGG ATGCTCCTGC TGTCACAGTG AGATATTACA GGATCACTTA CGGAGAAACA 660
GGAGGAAATA GCCCTGTCCA GGAGTTCACT GTGCCTGGGA GCAAGTCTAC AGCTACCATC 720
AGCGGCCCTTA AACCTGGAGT TGATTATAACC ATCACTGTGT ATGCTGTCAC TGGCCGTGGA 780
GACAGCCCCG CAAGCAGCAA GCCAATTCC ATTAATTACC GAACAGAAAT TGACAAACCA 840
10 TCCACTAGCG CTATTCTGC ACCAACTGAC CTGAAGTTCA CTCAGGTAC ACCCACAAGC 900
CTGAGCGCCC AGTGGACACC ACCCAATGTT CAGCTCACTG GATATCGAGT GCGGGTGACC 960
CCCAAGGAGA AGACCGGACC AATGAAAGAA ATCAACCTG CTCCTGACAG CTCATCCGTG 1020
GTTGTATCAG GACTTATGGT GGCCACCAAA TATGAAGTGA GTGTCTATGC TCTTAAGGAC 1080
ACTTTGACAA GCAGACCAGC TCAGGGTGT GTCACCACTC TGGAGAATGT CAGCCCACCA 1140
15 AGAAGGGCTC GTGTGACAGA TGCTACTGAG ACCACCATCA CCATTAGCTG GAGAACCAAG 1200
ACTGAGACGA TCACTGGCTT CCAAGTTGAT GCCGTTCCAG CCAATGCCA GACTCCAATC 1260
CAGAGAACCA TCAAGCCAGA TGTCAAGAGC TACACCATCA CAGGTTTACA ACCAGGCAC 1320
GACTACAAGA TCTACCTGTA CACCTTGAAT GACAATGCTC GGAGCTCCCC TGTGGTCATC 1380
GACGCCCTCCA CTGCCATTGA TGCACCATCC AACCTGCGTT TCCTGGCCAC CACACCAAT 1440
20 TCCTTGCTGG TATCATGGCA GCCGCCACGT GCCAGGATTA CCGGCTACAT CATCAAGTAT 1500
GAGAAGCCTG GGTCTCCTCC CAGAGAAGTG GTCCCTCGGC CCCGCCCTGG TGTCACAGAG 1560
GCTACTATTA CTGGCCTGGA ACCGGGAACC GAATATACAA TTTATGTCAT TGCCCTGAAG 1620
AATAATCAGA AGAGCGAGCC CCTGATTGGA AGGAAAAAGA CTAGCGCTAT TCCTGCACCA 1680
ACTGACCTGA AGTTCACTCA GGTCACACCC ACAAGCCTGA GCGCCAGTG GACACCACCC 1740
25 AATGTTCAGC TCACTGGATA TCGAGTGCAG GTGACCCCCA AGGAGAAGAC CGGACCAATG 1800

AAAGAAATCA ACCTTGCTCC TGACAGCTCA TCCGTGGTTG TATCAGGACT TATGGTGGCC 1960
ACCAAATATG AAGTGAGTGT CTATGCTCTT AAGGACACTT TGACAAGCAG ACCAGCTCAG 1920
GGTGTGTCAGC CCACCTCTGGA GAATGTCAGC CCACCAAGAA GGGCTCGTGT GACAGATGCT 1980
ACTGAGACCA CCATCACCAT TAGCTGGAGA ACCAAGACTG AGACGATCAC TGGCTTCCAA 2040
5 GTTGATGCCG TTCCAGCCAA TGGCCAGACT CCAATCCAGA GAACCATCAA GCCAGATGTC 2100
AGAAGCTACA CCATCACAGG TTTACAACCA GGCAGTACT ACAAGATCTA CCTGTACACC 2160
TTGAATGACA ATGCTCGGAG CTCCCCCTGTG GTCATCGACG CCTCCACTGC CATTGATGCA 2220
CCATCCAACC TGCCTTCCCT GGCCACCACA CCCAATTCCCT TGCTGGTATC ATGGCAGCCG 2280
CCACGTGCCA GGATTACCGG CTACATCATC AAGTATGAGA AGCCTGGGTC TCCTCCCAGA 2340
GAAGTGGTCC CTCGGCCCCG CCCTGGTGTG ACAGAGGCTA CTATTACTGG CCTGGAACCG 2400
GGAACCGAAT ATACAATTAA TGTCATTGCC CTGAAGAATA ATCAGAAGAG CGAGCCCCCTG 2460
ATTGGAAGGA AAAAGACTAG T 2481

SEQ. ID No. 21

LENGTH: 472

15 TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

20 Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

| | | | |
|----|---|-----|-----|
| | 35 | 40 | 45 |
| | Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu | | |
| | 50 | 55 | 60 |
| | Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln | | |
| 5 | 65 | 70 | 75 |
| | His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp | | |
| | 80 | 85 | 90 |
| | Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe | | |
| | 95 | 100 | 105 |
| 10 | Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg | | |
| | 110 | 115 | 120 |
| | Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp | | |
| | 125 | 130 | 135 |
| 15 | Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr | | |
| | 140 | 145 | 150 |
| | Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg | | |
| | 155 | 160 | 165 |
| | Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp | | |
| | 170 | 175 | 180 |
| 20 | Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu | | |
| | 185 | 190 | 195 |
| | Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg | | |
| | 200 | 205 | 210 |
| | Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe | | |
| 25 | 215 | 220 | 225 |

Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys
230 235 240
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg
245 250 255
5 Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg
260 265 270
Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp
275 280 285
Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp
290 295 300
Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr
305 310 315
Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro
320 325 330
Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys
335 340 345
Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg
350 355 360
Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro
20 365 370 375
Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile
380 385 390
Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp
395 400 405
25 Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys

410 415 420
Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr
425 430 435
Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser
5 440 445 450
Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser
455 460 465
Asn Leu Arg Phe Leu Ala Thr
470

10 SEQ. ID No. 22

LENGTH: 457

15 TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

20 MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg
1 5 10 15
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
20 20 25 30
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
35 35 40 45
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu
50 50 55 60

Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln
65 70 75
His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp
80 85 90
5 Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe
95 100 105
Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg
110 115 120
Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp
125 130 135
Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr
140 145 150
Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg
155 160 165
Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp
170 175 180
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu
185 190 195
Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg
200 205 210
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
215 220 225
Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys
230 235 240
25 Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg

| | | | |
|----|---|-----|-----|
| | 245 | 250 | 255 |
| | Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg | | |
| | 260 | 265 | 270 |
| | Thr Glu Ile Asp Lys Pro Ser Met Asn Val Ser Pro Pro Arg Arg | | |
| 5 | 275 | 280 | 285 |
| | Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp | | |
| | 290 | 295 | 300 |
| | Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val | | |
| | 305 | 310 | 315 |
| 10 | Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp | | |
| | 320 | 325 | 330 |
| | Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr | | |
| | 335 | 340 | 345 |
| 15 | Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro | | |
| | 350 | 355 | 360 |
| | Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu | | |
| | 365 | 370 | 375 |
| | Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln | | |
| | 380 | 385 | 390 |
| 20 | Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys | | |
| | 395 | 400 | 405 |
| | Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly | | |
| | 410 | 415 | 420 |
| | Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr | | |
| 25 | 425 | 430 | 435 |

Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro
440 445 450
Leu Ile Gly Arg Lys Lys Thr
455

5 SEQ. ID No. 23

LENGTH: 549

10 TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

15 MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

35 40 45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu

50 55 60

20 Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

65 70 75

His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp

80 85 90

Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

| | | | |
|----|---|-----|-----|
| | 95 | 100 | 105 |
| | Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg | | |
| | 110 | 115 | 120 |
| | Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp | | |
| 5 | 125 | 130 | 135 |
| | Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr | | |
| | 140 | 145 | 150 |
| | Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg | | |
| | 155 | 160 | 165 |
| 10 | Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp | | |
| | 170 | 175 | 180 |
| | Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu | | |
| | 185 | 190 | 195 |
| | Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg | | |
| 15 | 200 | 205 | 210 |
| | Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe | | |
| | 215 | 220 | 225 |
| | Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys | | |
| | 230 | 235 | 240 |
| 20 | Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg | | |
| | 245 | 250 | 255 |
| | Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg | | |
| | 260 | 265 | 270 |
| | Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp | | |
| 25 | 275 | 280 | 285 |

Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp
290 295 300

Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr
305 310 315

5 Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro
320 325 330

Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys
335 340 345

Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg
350 355 360

10 Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro
365 370 375

Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile
380 385 390

15 Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp
395 400 405

Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys
410 415 420

Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr
20 425 430 435

Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser
440 445 450

25 Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser
455 460 465

Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser

| | | | | | |
|---|-----|--|-----|--|-----|
| | 470 | | 475 | | 480 |
| Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr | | | | | |
| | 485 | | 490 | | 495 |
| Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg | | | | | |
| | 500 | | 505 | | 510 |
| Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr | | | | | |
| | 515 | | 520 | | 525 |
| Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser | | | | | |
| | 530 | | 535 | | 540 |
| Glu Pro Leu Ile Gly Arg Lys Lys Thr | | | | | |
| | 545 | | | | |

SEQ. ID No. 24

LENGTH: 574

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

20 1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
35 40 45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu
50 55 60
Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln
65 70 75
5 His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp
80 85 90
Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe
95 100 105
Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg
110 115 120
Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp
125 130 135
Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr
140 145 150
155 160 165
Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg
Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp
170 175 180
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu
20 185 190 195
Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg
200 205 210
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
215 220 225
25 Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys

| | | | |
|----|---|-----|-----|
| | 230 | 235 | 240 |
| | Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg | | |
| | 245 | 250 | 255 |
| | Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg | | |
| 5 | 260 | 265 | 270 |
| | Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp | | |
| | 275 | 280 | 285 |
| | Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp | | |
| | 290 | 295 | 300 |
| 10 | Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr | | |
| | 305 | 310 | 315 |
| | Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro | | |
| | 320 | 325 | 330 |
| | Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys | | |
| 15 | 335 | 340 | 345 |
| | Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg | | |
| | 350 | 355 | 360 |
| | Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro | | |
| | 365 | 370 | 375 |
| 20 | Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile | | |
| | 380 | 385 | 390 |
| | Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp | | |
| | 395 | 400 | 405 |
| | Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys | | |
| 25 | 410 | 415 | 420 |

Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr
425 430 435
Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser
440 445 450
5 Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser
455 460 465
Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser
470 475 480
Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr
485 490 495
Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg
500 505 510
Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr
515 520 525
15 Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser
530 535 540
Glu Pro Leu Ile Gly Arg Lys Lys Thr Asp Glu Leu Pro Gln Leu
545 550 555
Val Thr Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp
20 560 565 570
Val Pro Ser Thr

SEQ. ID No. 25

LENGTH: 274

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

5 Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg
1 5 10 15
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
20 25 30
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
35 40 45
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu
50 55 60
Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln
65 70 75
15 His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp
80 85 90
Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe
95 100 105
Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg
20 110 115 120
Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp
125 130 135
Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr
140 145 150
25 Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg

155 160 165
Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp
170 175 180
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu
5 185 190 195
Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg
200 205 210
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
215 220 225
Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys
230 235 240
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg
245 250 255
Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg
260 265 270
Thr Glu Ile Asp

SEQ. ID No. 26

LENGTH: 1374

TYPE: nucleic acid

20 STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGCCCACTG ACCTGCGATT CACCAACATT GGTCCAGACA CCATGCGTGT CACCTGGCT 60
CCACCCCCAT CCATTGATTT AACCAACTTC CTGGTGCCTT ACTCACCTGT GAAAAATGAG 120
GAAGATGTTG CAGAGTTGTC AATTTCTCCT TCAGACAATG CAGTGGCTT AACAAATCTC 180
CTGCCTGGTA CAGAATATGT AGTGAGTGTC TCCAGTGTCT ACGAACAAACA TGAGAGCACA 240
5 CCTCTTAGAG GAAGACAGAA AACAGGTCTT GATTCCCCAA CTGGCATTGA CTTTCTGAT 300
ATTACTGCCA ACTCTTTAC TGTGCACTGG ATTGCTCCTC GAGCCACCAT CACTGGCTAC 360
AGGATCCGCC ATCATCCGA GCACTTCACT GGGAGACCTC GAGAAGATCG GGTGCCAAC 420
TCTCGGAATT CCATCACCCCT CACCAACCTC ACTCCAGGCA CAGAGTATGT GGTCAGCATE 480
GTTGCTCTTA ATGGCAGAGA GGAAAGTCCC TTATTGATTG GCCAACAAATC AACAGTTCT 540
GATGTTCCGA GGGACCTGGA AGTTGTTGCT GCGACCCCCA CCAGCCTACT GATCAGCTGG 600
GATGCTCCTG CTGTCACAGT GAGATATTAC AGGATCACTT ACGGAGAAC AGGAGGAAAT 660
AGCCCTGTCC AGGAGTCAC TGTGCCTGGG AGCAAGTCTA CAGCTACCAT CAGCGGCCTT 720
AAACCTGGAG TTGATTATAC CATCACTGTG TATGCTGTCA CTGGCCGTGG AGACAGCCCC 780
GCAAGCAGCA AGCCAATTTC CATTAATTAC CGAACAGAAA TTGACAAACC ATCCATGGCA 840
GCCGGGAGCA TCACCACGCT GCCCGCCTTG CCCGAGGATG GCGGCAGCGG CGCCTTCCCG 900
CCCGGCCACT TCAAGGACCC CAAGCGGCTG TACTGCAAAA ACGGGGGCTT CTTCTGCGC 960
ATCCACCCCG ACGGCCGAGT TGACGGGGTC CGGGAGAAGA GCGACCCCTCA CATCAAGCTA 1020
CAAATTCAAG CAGAAGAGAG AGGAGTTGTG TCTATCAAAG GAGTGTGTGC TAACCGTTAC 1080
CTGGCTATGA AGGAAGATGG AAGATTACTG GCTTCTAAAT GTGTTACGGA TGAGTGTTC 1140
20 TTTTTGAAC GATTGGAATC TAATAACTAC AATACTTACC GCTCAAGGAA ATACACCAGT 1200
TGGTATGTGG CACTGAAACG AACTGGGCAG TATAAACTTG GATCCAAAAC AGGACCTGGG 1260
CAGAAAGCTA TACTTTTCT TCCAATGTCT GCTGCTAGCG ACGAGCTTCC CCAACTGGTA 1320
ACCCCTCCAC ACCCAATCT TCATGGACCA GAGATCTTGG ATGTTCCCTTC CACA 1374

LENGTH: 1416

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

5 MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

CCCCACTGACC TCGGATTCAC CAACATTGGT CCAGACACCA TGCCTGTCAC CTGGGCTCCA 60
CCCCCATCCA TTGATTTAAC CAACTTCCTG GTGCGTTACT CACCTGTGAA AAATGAGGAA 120
10 GATGTTGCAG AGTTGTCAAT TTCTCCTTCA GACAATGCAG TGGTCTTAAC AAATCTCCTG 180
CCTGGTACAG AATATGTAGT GAGTGTCTCC AGTGTCTACG AACAAACATGA GAGCACACCT 240
CTTAGAGGAA GACAGAAAAC AGGTCTTGAT TCCCCAACTG GCATTGACTT TTCTGATATT 300
ACTGCCAACT CTTTACTGT GCACTGGATT GCTCCTCGAG CCACCATCAC TGGCTACAGG 360
ATCCGCCATC ATCCCGAGCA CTTCAGTGGG AGACCTCGAG AAGATCGGGT GCCCCACTCT 420
15 CGGAATTCCA TCACCCCTCAC CAACCTCACT CCAGGCACAG AGTATGTGGT CAGCATCGTT 480
GCTCTTAATG GCAGAGAGGA AAGTCCCTTA TTGATTGGCC ACAAATCAAC AGTTTCTGAT 540
GTTCCGAGGG ACCTGGAAGT TGTTGCTGCG ACCCCCACCA GCCTACTGAT CAGCTGGGAT 600
GCTCCTGCTG TCACAGTGAG ATATTACAGG ATCACTTACG GAGAAACAGG AGGAAATAGC 660
CCTGTCCAGG AGTTCACTGT GCCTGGGAGC AAGTCTACAG CTACCATCAG CGGCCTTAAA 720
20 CCTGGAGTTG ATTATACCAT CACTGTGTAT GCTGTCACTG GCCGTGGAGA CAGCCCCGCA 780
AGCAGCAAGC CAATTTCCAT TAATTACCGA ACAGAAATTG ACAAAACCATC CATGGCTATT 840
CCTGCACCAA CTGACCTGAA GTTCACTCAG GTCACACCCA CAAGCCTGAG CGCCCAGTGG 900
ACACCCACCA ATGTTCAGCT CACTGGATAT CGAGTGCGGG TGACCCCCAA GGAGAAAGACC 960
GGACCAATGA AAGAAATCAA CCTTGCTCCT GACAGCTCAT CCGTGGTTGT ATCAGGACTT 020
25 ATGGTGGCCA CCAAATATGA AGTGAGTGTC TATGCTCTTA AGGACACTTT GACAAGCAGA 1080

CCAGCTCAGG GTGTTGTCAC CACTCTGGAG AATGTCAGCC CACCAAGAAG GGCTCGTGTG 1140
ACAGATGCTA CTGAGACCAAC CATCACCAATT AGCTGGAGAA CCAAGACTGA GACGATCACT 1200
GGCTTCCAAG TTGATGCCGT TCCAGCCAAT GGCCAGACTC CAATCCAGAG AACCATCAAG 1260
CCAGATGTCA GAAGCTACAC CATCACAGGT TTACAACCAG GCACTGACTA CAAGATCTAC 1320
5 CTGTACACCT TGAATGACAA TGCTCGGAGC TCCCCTGTGG TCATCGACGC CTCCACTGCC 1380
ATTGATGCAC CATCCAACCT GCGTTTCCTG GCCACC 1416

SEQ. ID No. 28

LENGTH: 35

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly Gln Arg

15 1 5 10 15

Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly Ile Thr

20 20 25 30

Gly Lys Pro Gly Pro

35

20 SEQ. ID No. 29

LENGTH: 302

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

5 1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

35 40 45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu

50 55 60

Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

65 70 75

His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp

80 85 90

Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

95 100 105

Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg

110 115 120

20 Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp

125 130 135

Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr

140 145 150

Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg

25 155 160 165

Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp
170 175 180
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu
185 190 195
5 Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg
200 205 210
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
215 220 225
10 Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys
230 235 240
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg
245 250 255
Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg
260 265 270
15 Thr Glu Ile Asp Lys Pro Ser Asp Glu Leu Pro Gln Leu Val Thr
275 280 285
Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro
290 295 300
20 Ser Thr

SEQ. ID No. 30

LENGTH: 573

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Met Ala Ala Ser Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr

5 5 10 15

5 Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn
20 25 30

Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu Lys
35 40 45

Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser
50 55 60

Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser
65 70 75

Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly
80 85 90

Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg
95 100 105

Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr
110 115 120

Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala
20 125 130 135

Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val Arg
140 145 150

Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile
155 160 165

25 Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val

170 175 180
Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe
185 190 195
Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro
5 200 205 210
Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly
215 220 225
Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr
230 235 240
Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile
245 250 255
Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile
260 265 270
Gly Arg Lys Lys Thr Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe
275 280 285
Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro
290 295 300
Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu
305 310 315
20 Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser
320 325 330
Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val
335 340 345
Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln
25 350 355 360

Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala
365 370 375

Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg
380 385 390

5 Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro
395 400 405

Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val
410 415 420

Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys
425 430 435

Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val
440 445 450

Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg
455 460 465

15 Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro
470 475 480

Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro
485 490 495

Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val
20 500 505 510

Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr
515 520 525

Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu
530 535 540

25 Ile Gly Arg Lys Lys Thr Ser Asp Glu Leu Pro Gln Leu Val Thr

545 550 555
Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro
560 565 570
Ser Thr Ser

5 SEQ. ID No. 31

LENGTH: 37

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

10 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCAAT GTCAGCCCAC CAAGAAG

37

SEQ. ID No. 32

LENGTH: 37

15 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

20 AAAGGATCCC TAACTAGTGG AAGGAACATC CAAGATC

37

SEQ. ID No. 33

LENGTH: 1722

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial
5 polypeptide)

SEQUENCE:

ATGGCAGCTA GCGCTATTCC TGCACCAACT GACCTGAAGT TCACTCAGGT CACACCCACA 60
AGCCTGAGCG CCCAGTGGAC ACCACCCAAT GTTCAGCTCA CTGGATATCG AGTGCAGGGTG 120
ACCCCCAAGG AGAAGACCGG ACCAATGAAA GAAATCAACC TTGCTCCTGA CAGCTCATCC 180
10 GTGGTTGTAT CAGGACTTAT GGTGGCCACC AAATATGAAG TGAGTGTCTA TGCTCTTAAG 240
GACACTTTGA CAAGCAGACC AGCTCAGGGT GTTGTACCCA CTCTGGAGAA TGTCAGCCC 300
CCAAGAAGGG CTCGTGTGAC AGATGCTACT GAGACCACCA TCACCATTAG CTGGAGAAC 360
AAGACTGAGA CGATCACTGG CTTCCAAGTT GATGCCGTT CAGCCAATGG CCAGACTCCA 420
ATCCAGAGAA CCATCAAGCC AGATGTCAGA AGCTACACCA TCACAGGTTT ACAACCAGGC 480
15 ACTGACTACA AGATCTACCT GTACACCTTG AATGACAATG CTCGGAGCTC CCCTGTGGTC 540
ATCGACGCCCT CCACTGCCAT TGATGCACCA TCCAACCTGC GTTCCCTGGC CACCACACCC 600
AATTCCCTTGC TGGTATCATG GCAGCCGCCA CGTGCCAGGA TTACCGGCTA CATCATCAAG 660
TATGAGAAGC CTGGGTCTCC TCCCAGAGAA GTGGTCCCTC GGCCCCGCC CGGTGTACCA 720
GAGGCTACTA TTACTGGCCT GGAACCGGGA ACCGAATATA CAATTTATGT CATTGCCCTG 780
20 AAGAATAATC AGAAGAGCGA GCCCCTGATT GGAAGGAAAA AGACTAGCGC TATTCCCTGCA 840
CCAACTGACC TGAAGTTCAC TCAGGTACCA CCCACAAGCC TGAGCGCCCA GTGGACACCA 900
CCCAATGTTG AGCTCACTGG ATATCGAGTG CGGGTGACCC CCAAGGAGAA GACCGGACCA 960
ATGAAAGAAA TCAACCTTGC TCCTGACAGC TCATCCGTGG TTGTATCAGG ACTTATGGTG 1020
GCCACCAAAT ATGAAGTGAG TGTCTATGCT CTTAAGGACA CTTTGACAAG CAGACCAGCT 1080
25 CAGGGTGTG TCACCACTCT GGAGAATGTC AGCCCCACCAA GAAGGGCTCG TGTGACAGAT 1140

100
5 GCTACTGAGA CCACCATCAC CATTAGCTGG AGAACCAAGA CTGAGACGAT CACTGGCTTC 1200
CAAGTTGATG CCGTTCCAGC CAATGGCCAG ACTCCAATCC AGAGAACCAT CAAGCCAGAT 1260
GTCAGAAGCT ACACCATCAC AGGTTACAA CCAGGCAC TG ACTACAAGAT CTACCTGTAC 1320
ACCTTGAATG ACAATGCTCG GAGCTCCCCT GTGGTCATCG ACGCCTCCAC TGCCATTGAT 1380
15 GCACCATCCA ACCTGCGTTT CCTGGCCACC ACACCCAATT CCTTGCTGGT ATCATGGCAG 1440
CCGCCACGTG CCAGGATTAC CGGCTACATC ATCAAGTATG AGAACGCTGG GTCTCCTCCC 1500
AGAGAAGTGG TCCCTCGGCC CCGCCCTGGT GTCACAGAGG CTACTATTAC TGGCCTGGAA 1560
CCGGGAACCG AATATACAAT TTATGTCATT GCCCTGAAGA ATAATCAGAA GAGCGAGCCC 1620
CTGATTGGAA GGAAAAAGAC TAGCGACGAG CTTCCCCAAC TGGTAACCCT TCCACACCCCC 1680
AATCTTCATG GACCAGAGAT CTTGGATGTT CCTTCCACTA GT 1722

SEQ. ID No. 34

LENGTH: 412

TYPE: amino acid

STRANDEDNESS: single

15 TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln
5 10 15
20 Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
20 25 30
His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys
35 40 45
Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp

| | | | |
|----|---|-----|-----|
| | 50 | 55 | 60 |
| | Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile | | |
| | 65 | 70 | 75 |
| | Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala | | |
| 5 | 80 | 85 | 90 |
| | Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly | | |
| | 95 | 100 | 105 |
| | Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val | | |
| | 110 | 115 | 120 |
| 10 | Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp | | |
| | 125 | 130 | 135 |
| | Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His | | |
| | 140 | 145 | 150 |
| | Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met | | |
| 15 | 155 | 160 | 165 |
| | Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys | | |
| | 170 | 175 | 180 |
| | Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser | | |
| | 185 | 190 | 195 |
| 20 | Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe | | |
| | 200 | 205 | 210 |
| | Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ile Glu Gly Arg | | |
| | 215 | 220 | 225 |
| | Gly Ile Pro Arg Asn Ser Gly Ala Pro Pro Arg Leu Ile Cys Asp | | |
| 25 | 230 | 235 | 240 |

Ser Arg Val Leu Gln Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
245 250 255
Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
260 265 270
5 Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
275 280 285
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
290 295 300
Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn
305 310 315
Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
320 325 330
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
335 340 345
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
350 355 360
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg
365 370 375
Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly
20 380 385 390
Glu Ala Cys Arg Thr Gly Asp Arg Leu Ala Met Asp Pro Leu Glu
395 400 405
Ser Thr Arg Ala Ala Ala Ser
410

SEQ. ID No. 35

LENGTH: 24

TYPE: nucleic acid

STRANDEDNESS: single

5 TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GCTCCCTCTG GGCCTCCAG TCCT

24

SEQ. ID No. 36

LENGTH: 24

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GTTGGTGAGG GAGGTGGTGG ATAT

24

SEQ. ID No. 37

LENGTH: 33

TYPE: nucleic acid

20 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GGCCTCCCGA ATTCCGGTGC CCCACCACGC CTC

33

SEQ. ID No. 38

LENGTH: 33

TYPE: nucleic acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

CCCACGTGGA TCCATGGCTA ATCTGTCCCC TGT

33

10 SEQ. ID No. 39

LENGTH: 1239

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

15 MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGTCCCCTA TACTAGGTTA TTGGAAAATT AAGGGCCTTG TGCAACCCAC TCGACTTCTT 60

TTGGAATATC TTGAAGAAAA ATATGAAGAG CATTGTATG AGCGCGATGA AGGTGATAAA 120

20 TGGCGAAACA AAAAGTTGA ATTGGGTTTG GAGTTCCCA ATCTTCCTTA TTATATTGAT 180

GGTGATGTTA AATTAACACA GTCTATGCC ATCATACTGTT ATATAGCTGA CAAGCACAAC 240

ATGTTGGGTG GTTGTCCAAA AGAGCGTGCA GAGATTCAA TGCTTGAAGG AGCGGTTTG 300

GATATTAGAT ACGGTGTTTC GAGAATTGCA TATAGTAAAG ACTTTGAAAC TCTCAAAGTT 360

| | | |
|----|--|------|
| 5 | GATTTCTTA GCAAGCTACC TGAAATGCTG AAAATGTTCG AAGATCGTTT ATGTCATAAA | 420 |
| | ACATATTAA ATGGTGATCA TGTAACCCAT CCTGACTTCA TGTTGTATGA CGCTCTTGAT | 480 |
| | GTTGTTTAT ACATGGACCC AATGTGCCTG GATGCGTTCC CAAAATTAGT TTGTTTAAA | 540 |
| | AAACGTATTG AAGCTATCCC ACAAAATTGAT AAGTACTTGA AATCCAGCAA GTATATAGCA | 600 |
| | TGGCCTTGCA AGGGCTGGCA AGCCACGTTT GGTGGTGGCG ACCATCCTCC AAAATCGGAT | 660 |
| | CTGATCGAAG GTCGTGGAT CCCCAGGAAT TCCGGTGCCTC CACCACGCCT CATCTGTGAC | 720 |
| | AGCCGAGTCC TGCAGAGGTA CCTCTTGGAG GCCAAGGAGG CCGAGAATAT CACGACGGGC | 780 |
| | TGTGCTGAAC ACTGCAGCTT GAATGAGAAT ATCACTGTCC CAGACACCAA AGTTAATTTC | 840 |
| | TATGCCTGGA AGAGGATGGA GGTCGGGCAG CAGGCCGTAG AAGTCTGGCA GGGCCTGGCC | 900 |
| | CTGCTGTCGG AAGCTGTCCT GCAGGGCCAG GCCCTGTTGG TCAACTCTTC CCAGCCGTGG | 960 |
| | GAGCCCTGC AGCTGCATGT GGATAAAGCC GTCAGTGGCC TTCGCAGCCT CACCACTCTG | 1020 |
| | CTTCGGGCTC TGGGAGGCCA GAAGGAAGCC ATCTCCCCTC CAGATGCCGC CTCAGCTGCT | 1080 |
| | CCACTCCGAA CAATCACTGC TGACACTTTC CGCAAACCTCT TCCGAGTCTA CTCCAATTTC | 1140 |
| | CTCCGGGAA AGCTGAAGCT GTACACAGGG GAGGCCTGCA GGACAGGGGA CAGATTAGCC | 1200 |
| 15 | ATGGATCCTC TAGAGTCGAC TCGAGCGGCC GCATCGTGA | 1239 |